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OIPE

pp 1-24

```
 2 <110> APPLICANT: Corvas International , Inc.
 3        Vlasuk, George Phillip
 4        Stanssens, Patrick Eric Hugo
 5        Messens, Joris Hila Lieven
 6        Lauwereys, Marc Josef
 7        Laroche, Yves Rene
 8        Jespers, Laurent Stephane
 9        Gansemans, Yannick Georges Jozef
10        Moyle, Matthew
11        Bergum, Peter W.
13 <120> TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND
ANTICOAGULANT
14        PROTEIN
16 <130> FILE REFERENCE: 018813/0272487
18 <140> CURRENT APPLICATION NUMBER: 09/498,556A
19 <141> CURRENT FILING DATE: 2002-04-10
21 <150> PRIOR APPLICATION NUMBER: 08/809,455
22 <151> PRIOR FILING DATE: 1997-04-17
24 <150> PRIOR APPLICATION NUMBER: PCT/US95/13231
25 <151> PRIOR FILING DATE: 1995-10-17
27 <150> PRIOR APPLICATION NUMBER: 08/486,399
28 <151> PRIOR FILING DATE: 1995-06-05
30 <150> PRIOR APPLICATION NUMBER: 08/486,397
31 <151> PRIOR FILING DATE: 1995-06-05
33 <150> PRIOR APPLICATION NUMBER: 08/465,380
34 <151> PRIOR FILING DATE: 1995-06-05
36 <150> PRIOR APPLICATION NUMBER: 08/461,965
37 <151> PRIOR FILING DATE: 1995-06-05
39 <150> PRIOR APPLICATION NUMBER: 08/326,110
40 <151> PRIOR FILING DATE: 1994-10-18
42 <160> NUMBER OF SEQ ID NOS: 356
44 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

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61 <210> SEQ ID NO: 2
62 <211> LENGTH: 228
63 <212> TYPE: DNA
64 <213> ORGANISM:
66 <400> SEQUENCE: 2
68 aaggcatacc cggagtgtgg tgagaatgaa tggctcgacg tctgtggaac taagaagcca 60
70 tgcgaggcca agtgcagtga ggaagaggag gaagatccga tatgccgatc attttcttgt 120
72 ccgggtcccg ctgcttgcgt atgcgaagac ggattctaca gagacacggt gatcggcgac 180
```

4/26/02

RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
    74 tgtgttaagg aagaagaatg cgaccaacat gagattatac atgtctga 228
    76 <210> SEQ ID NO: 3
    77 <211> LENGTH: (461)  460?
    78 <212> TYPE: DNA
    79 <213> ORGANISM: Ancyclostoma caninum
    81 <220> FEATURE:
    82 <221> NAME/KEY: CDS
    83 <222> LOCATION: (22)..(321)
    85 <220> FEATURE:
    86 <221> NAME/KEY: misc_feature
    87 <223> OTHER INFORMATION:
    89 <400> SEQUENCE: 3
C--> 91 gaattccgct actactcaac a atg aag atg ctt tac gct atc gct ata atg  51
    92         Met Lys Met Leu Tyr Ala Ile Ala Ile Met
W--> 93      1 5 10
E--> 94 ttt ctc ctg gta tca tta tgc agc gca aga aca gtg ag(C) aag gca tac 99
    95 Phe Leu Leu Val Ser Leu Cys Ser Ala Arg Thr Val Arg Lys Ala Tyr
W--> 96     15 20 25
    97 ccg gag tgt ggt gag rat gaa tgg ctc gac gac tgt gga act cag aag 147
W--> 98 Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp Cys Gly Thr (Gln) Lys
W--> 99    30 35 40
E--> 100 cca tgc gag (Gcc aag tgc rat gag gra ccc cct gag gag gaa (Gat ccg (195 ?)
    101 Pro Cys Glu Ala Lys Cys Asn Glu Glu Pro Pro Glu Glu Glu Asp Pro
W--> 102   45 50 55
E--> 103 ata tgc cgc tca cgt g(C)t tgt tta tta cct cct gct tgc gta tgc aaa  243
    104 Ile Cys Arg Ser Arg Gly Cys Leu Leu Pro Pro Ala Cys Val Cys Lys
W--> 105   60 65 70
E--> 106 gac (Cga ttc tac aga gac a(Cg (OtO) atc ggc gac t(Ot gtt ag(C) gaa gaa  291
W--> 107 Asp Gly Phe Tyr Arg Asp Tsr Val Ile Oly Asp Cys Val Arg Glu Glu
W--> 108   75 80 85 90
E--> 109 gaa t(Cc gac car cat gag att ata cat gtc t gaacgagaaa gcaacaataa cc  344
W--> 110 Glu Cys Asp (Gln His Glu Ile Ile His Val
W--> 111   95 100
E--> 112 aaaggttcca actctcgctc tgcaaaatcg ctagttg(Oat gtctcttttg cgtccgaata 404
E--> 114 gttttagttg atgttaagta agaactcctg ctggagagaa taaagctttc caactcc (461 ?)
    116 <210> SEQ ID NO: 4
    117 <211> LENGTH: 77
    118 <212> TYPE: PRT
    119 <213> ORGANISM: Ascyclostoma caninum
    121 <400> SEQUENCE: 4
    123 Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp
E--> 124   1 5 10
    125 Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu Glu
E--> 126  15 20          25
    127 Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly Cys
E--> 128  30 35          40
    129 Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg
E--> 130          45               50               55
    131 Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu Glu Cys Asp
```

[Handwritten annotations:]
- use lower-case letters for all bases
- move over — amino acids must be under respective codons
- do not use tab codes
- invalid
- misaligned nos. see item 3 on Error Summary Sheet
- misaligned
- invalid
- These types of error are global. Please edit globally.
- misaligned amino acid nos. (see item 3 on Error Summary Sheet)

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Input Set : **A:\PTO.VSK.txt**
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```
E--> 132        60              65            70        misaligned
     133 Gln His Glu Ile Ile His Val                    amino acid nos.
E--> 134            75
     214 <210> SEQ ID NO: 8
     215 <211> LENGTH: 79
     216 <212> TYPE: PRT
     217 <213> ORGANISM: Ascyclostoma caninum
     219 <400> SEQUENCE: 8
     221 Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu
     222 1               5               10              15
     223 Asp Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu
     224             20              25              30
     225 Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly Pro Ala
     226         35              40              45
     227 Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp
     228     50              55              60
E--> 229 Cys Val Lys Glu Glu Glu Cys Asp Gln His Glu Ile Ile His Val
     230 65              70              75
     291 <210> SEQ ID NO: 10
     292 <211> LENGTH: 425
     293 <212> TYPE: DNA
     294 <213> ORGANISM: Ancyclostoma ceylanicum
     296 <220> FEATURE:
     297 <221> NAME/KEY: CDS (10)  <-- Coding starts at location 10
     298 <222> LOCATION: (1)..(291)
     300 <220> FEATURE:
     301 <221> NAME/KEY: misc_feature
     302 <223> OTHER INFORMATION:
     304 <400> SEQUENCE: 10
C--> 306 gaattccgc atg cgg acg ctc tac ctc att tct atc tgg ttg ttc ctc atc 51
     307       Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu Phe Leu Ile
     308       1           5               10
     309 tcg car tgt art gga aaa gga ttc ccg aaa tgt gac gtc art gaa aga 99
     310 Ser Gln Cys Asn Gly Lys Ala Phe Pro Lys Cys Asp Val Asn Gln Arg
     311 15          20              25              30
E--> 312 ttc ga(0) gtg tgt ggc art ctg aag gag tgc gag ctc aag tgc gat gag 147
     313 Phe Gln Val Cys Gly Asn Leu Lys Glu Cys Glu Leu Lys Cys Asp Glu
     314             35              40              45
     315 gac cct aag ata tgc tct cgt gca tgt att cgt ccc cct gct tgc gta 195
     316 Asp Pro Lys Ile Cys Ser Arg Ala Cys Ile Arg Pro Pro Ala Cys Val
W--> 317 (50 55 60  misaligned nos. (see item 3)
     318 tgc gat gac gga ttc tac aga gac aaa tat ggc ttc tgt gtt gaa gaa 243
     319 Cys Asp Asp Gly Phe Tyr Arg Asp Lys Tyr Gly Phe Cys Val Gln Gln
W--> 320 (65 70 75  misaligned nos.
     321 gac gaa tgt aac gat atg gag att att act ttt cca cca gaa acc aaa tg 293
     322 Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Gln Thr Lys
W--> 323 (80 85 90  misaligned nos.
     325 atgaccgaag cttccacctt tctatacata tcttcactgc ttgacaggct tctcgacaat 353
     327 ttagaagttc tgcttgactt tgtctatttg aaattgttca cactartggg ggaagtaaag 413
```

(handwritten annotations:) this is an upper-case "I"; invalid; use lower-case letters; invalid

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Input Set : A:\PTO.VSK.txt
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```
329 cattttcacg ac 425
413 <210> SEQ ID NO: 13
414 <211> LENGTH: 688
415 <212> TYPE: DNA
416 <213> ORGANISM: Ancyclostoma ceylanicum
418 <220> FEATURE:
419 <221> NAME/KEY: CDS
420 <222> LOCATION: (21)..(560)
422 <220> FEATURE:
423 <221> NAME/KEY: misc_feature
424 <223> OTHER INFORMATION:
426 <400> SEQUENCE: 13
```

use lower-case letters for bases

```
C-->  429 gaattccggg cggcagaaag  atg cga atg ctc tac ctt gtt cct atc tgg 50
      430                       Met Arg Met Leu Tyr Leu Val Pro Ile Trp
```
→ *move under respective codons*
```
W-->  431  1  5  10
```
m-modified nos.
```
      432 ttg ctg ctc att tcg cta tgc agt gga aaa gct gcg aag aaa tgt ggt 98
      433 Leu Leu Leu Ile Ser Leu Cys Ser Gly Lys Ala Ala Lys Lys Cys Gly
W-->  434 15 20 25
      435 ctc aat gaa agg ctg gac tgt ggc aat ctg aag caa tgc gag ccc aag 146
      436 Leu Asn Glu Arg Leu Asp Cys Gly Asn Leu Lys Gln Cys Glu Pro Lys
W-->  437 30 35 40
      438 tgc agc gac ttg gaa agt gag gag tat gag gag gaa gat gag tcg aaa 194
      439 Cys Ser Asp Leu Glu Ser Glu Glu Tyr Glu Glu Glu Asp Glu Ser Lys
W-->  440 45 50 55
      441 tgt cga tca cgt gaa tgt tct cgt cgt gtt tgt gta tgc gat gaa gga 242
W-->  442 Cys Arg Ser Arg Glu Cys Ser Arg Arg Val Syc Val Syc Asp Glu Gly
W-->  443 60      65 70
```
invalid
```
      444 ttc tac aga aac aag aag ggc aag tgt gtt cga aaa gat gtt tgc gag 290
      445 Phe Tyr Arg Asn Lys Lys Gly Lys Cys Val Ala Lys Asp Val Cys Glu
W-->  446 75 80 85 90
      447 gac gac aat atg gag att atc act ttt cca cca gaa gac gaa tgt ggt 338
      448 Asp Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Glu Cys Gly
W-->  449 95 100 105
      450 ccc gat gaa tgg ttc gac tac tgt gga aat tat aag aag tgc gaa cgc 386
      451 Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr Lys Lys Cys Glu Arg
W-->  452         110 115 120
      453 aag tgc agt gag gag aca agt gag aaa aat gag gag gca tgc ctc tct 434
      454 Lys Cys Ser Glu Glu Thr Ser Glu Lys Asn Glu Glu Ala Cys Leu Ser
W-->  455 125 130 135
      456 cgt gct tgt act ggt cgt gct tgc gta tgc aaa gac gga ttg tac aga 482
      457 Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Lys Asp Gly Leu Tyr Arg
W-->  458 140 145 150
E-->  459 gac gac ttt ggc aac tgt gtt cca cat gac gaa tgc aac gat atg gag 530
      460 Asp Asp Phe Gly Asn Cys Val Pro His Asp Glu Cys Asn Asp Met Glu
W-->  461 155 160 165 170
      462 atc atc act ttt cca ccg gaa acc aaa cat tgaccagagg ctccaactct cgct 584
      463 Ile Ile Thr Phe Pro Pro Glu Thr Lys His
W-->  464 175     180
      465 acacaacgtc aggctagaa tggcccctct gcgagttagt agttttgctt gactctgctt 644
```
530 ← insert

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```
467 atttgagcac tttctattga tggcgaaaat aaagcattta aaac 688
469 <210> SEQ ID NO: 14
470 <211> LENGTH: (349) 301
471 <212> TYPE: DNA
472 <213> ORGANISM: Heligmosomoides polygyrus
474 <220> FEATURE:
475 <221> NAME/KEY: CDS
476 <222> LOCATION: (49)..(276)
478 <220> FEATURE:
479 <221> NAME/KEY: misc_feature
480 <223> OTHER INFORMATION:
482 <400> SEQUENCE: 14
```

use lower-case letter for bases ✓

```
C--> 484 gaattccgcg cacctgagag gtgagctacg caagtcttcg ctggtaca atg atc cga 57
     485  Met Ile Arg
     486  1                     move under codens
E--> 487 aag ctc gtt ctg act gct atc gtc acg gtg gtg cta agt gcg aag (105) 102
     488 Lys Leu Val Leu Thr Ala Ile Val Thr Val Val Leu Ser Ala Lys
W--> 489 (5  10  15)  misaligned nos.
E--> 490 acc tgt gga cca aac gag gag tac act gaa tgc ggg acg cca tgc gag (153)
     491 Thr Cys Gly Pro Asn Glu Glu Tyr Thr Glu Cys Gly Thr Pro Cys Glu    nos. off
W--> 492 (20  25  30  35)
E--> 493 ccg aag tgc aat gaa ccg atg cca gac atc tgt act ctg aac tgc atc (201)
     494 Pro Lys Cys Asn Glu Pro Met Pro Asp Ile Cys Thr Leu Asn Cys Ile
W--> 495 (40  45  50)
E--> 496 gtg aac gtg tgt cag tgc aaa ccc ggc ttc aag cgc gga ccg aaa gga (249)
     497 Val Asn Val Cys Gln Cys Lys Pro Gly Phe Lys Arg Gly Pro Lys Gly
W--> 498 (55  60  65)
E--> 499 tgc gtc gcc ccc gga cca ggc tgt aaa tagttctcca cctgcccttt cgttggaa (304)
     500 Cys Val Ala Pro Gly Pro Gly Cys Lys
E--> 501          70                    75
     588 <210> SEQ ID NO: 17
     589 <211> LENGTH: (425) 434
     590 <212> TYPE: DNA
     591 <213> ORGANISM: Heligmosomoides polygyrus
     593 <220> FEATURE:
     594 <221> NAME/KEY: CDS    (40) <— Coding begins at location 40
     595 <222> LOCATION: (1)..(291)
     597 <220> FEATURE:
     598 <221> NAME/KEY: misc_feature
     599 <223> OTHER INFORMATION:
     601 <400> SEQUENCE: 17
```

use lower-case letter for bases ✓

```
C--> 603 aagctttgct aacatactgc gtaataagga gtcttaatc atg cca gtt ctt ttg 54
W--> 604                                           Met Pro Val Leu Leu
     605                                           1               5
     606 ggt att ccg tta tta ttg cgt ttc ctc ggt ttc ctt ctg gta act ttg 102
     607 Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu Leu Val Thr Leu
     608                    10              15              20
     609 ttc ggc tat ctg ctt act ttc ctt aaa aag ggc ttc ggt aag ata gct 150
W--> 610 (Phe) Gly Tyr Leu Leu Thr Phe Leu Lys Lys Gly Phe Gly Lys Ile Ala
```

invalid

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```
611               25                30                35
612 att gct att tca ttg ttt ctt gct ctt att att ggg ctt aac tca att 198
613 Ile Ala Ile Ser Leu Phe Leu Ala Leu Ile Ile Gly Leu Asn Ser Ile
614               40                45                50
615 ctt gtg ggt tat ctc tct gat att agc gca caa tta ccc tct gat ttt 246
616 Leu Val Gly Tyr Leu Ser Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe
617               55                60                65
618 gtt cag ggc gtt cag tta att ctc ccg tct aat gcg ctt ccc tgt ttt 294
619 Val Gln Gly Val Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe
620 70                75                80                85
621 tat gtt att ctc tct gta aag gct gct att ttc att ttt gac gtt aaa 342
622 Tyr Val Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys
623               90                95                100
624 caa aaa atc gtt tct tat ttg gat tgg gat aaa ggt gga ggc tca ggc 390
625 Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly Ser Gly
626               105               110               115
627 gga tcggccaagt cggccatccc atatcacgcg gccgcggatc c 434
628 Gly
640 <210> SEQ ID NO: 19
641 <211> LENGTH: 425  430 (p.7)
642 <212> TYPE: DNA
643 <213> ORGANISM: Ancyclostoma ceylanicum
645 <220> FEATURE:
646 <221> NAME/KEY: CDS
647 <222> LOCATION: (10)..(282)
649 <220> FEATURE:
650 <221> NAME/KEY: "W" stands for A or T    This goes on ∠2237 line, since it
651 <223> OTHER INFORMATION:                 use lower-case letters for bases
653 <400> SEQUENCE: 19                                        Explains
655 gaattccgg ctg gtw tcc tac tgc agt gga aaa gca acg atg cag tgt ggt 51   use of
656           Leu Val Ser Tyr Cys Ser Gly Lys Ala Thr Met Gln Cys Gly     "W"
657           1             5                  10
658 gag aat gaa aag tac gat tcg tgc ggt agc aag gag tgc gat aag aag 99
659 Glu Asn Glu Lys Tyr Asp Ser Cys Gly Ser Lys Glu Cys Asp Lys Lys
660 15                20                25                30
661 tgc aaa tat gac gga gtt gag gag gaa gac gac gag gaa cct aat gtg 147
662 Cys Lys Tyr Asp Gly Val Glu Glu Glu Asp Asp Glu Glu Pro Asn Val
663               35                40                45
664 cca tgc cta gta cgt gtg tgt cat caa gat tgc gta tgc gaa gaa gga 195
665 Pro Cys Leu Val Arg Val Cys His Gln Asp Cys Val Cys Glu Glu Gly
666               50                55                60
667 ttc tat aga aac aaa gat gac aaa tgt gta tca gca gaa gag tgc gaa 243
668 Phe Tyr Arg Asn Lys Asp Asp Lys Cys Val Ser Ala Glu Asp Cys Glu
669               65                70                75
670 ctt gac aat atg gac ttt ata tat ccc gga act cga aac tgaacgaagg ctc 295
671 Leu Asp Asn Met Asp Phe Ile Tyr Pro Gly Thr Arg Asn
672 80                85                90
673 cattcttgct gcacaagatc gattgtctct cccctgcatc tcagtagttt tgctacattg 355
675 tatatggtag caaaaaatta gcttagggag aataaaatct ttacctatat ttaatcaatg 415
```

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Input Set : A:\PTO.VSK.txt
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```
E--> 677 aagtattctc tttct 430

     679 <210> SEQ ID NO: 20
     680 <211> LENGTH: 100
     681 <212> TYPE: PRT
     682 <213> ORGANISM: Ancyclostoma caninum
E--> 684 <400> SEQUENCE: (18) 20   change to
     686 Met Lys Met Leu Tyr Ala Ile Ala Ile Met Phe Leu Leu Val Ser Leu
     687  1               5                  10                  15
     688 Cys Ser Ala Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn
     689          20                  25                  30
     690 Glu Trp Leu Asp Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys
     691          35                  40                  45
     692 Asn Glu Glu Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly
     693          50                  55                  60
     694 Cys Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg Asp
     695 65                  70                  75                  80
     696 Thr Val Ile Gly Asp Cys Val Arg Glu Glu Glu Cys Asp Gln His Glu
     697                  85                  90                  95
     698 Ile Ile His Val
     699              100
E--> 762 <210> SEQ ID NO: 23
     763 <211> LENGTH: 96
     764 <212> TYPE: PRT                                    delete
     765 <213> ORGANISM: Ancyclostoma ceylanicum
     767 <400> SEQUENCE: 23
E--> 767 23
     868 <210> SEQ ID NO: 29
     869 <211> LENGTH: 76
     870 <212> TYPE: PRT
     871 <213> ORGANISM: Helogmosomoides polygyrus
     873 <400> SEQUENCE: 29
     875 Met Ile Arg Lys Leu Val Leu Leu Thr Ala Ile Val Thr Val Val Leu
     876  1               5                  10                  15
     877 Ser Ala Lys Thr Cys Gly Pro Asn Glu Glu Tyr Thr Glu Cys Gly Thr
     878          20                  25                  30
E--> 879 Pro Cys Glu Pro Lys Cys Asn Glu Pro Met Pro Asp Ile Cys Thr (Len) invalid
     880          35                  40                  45
     881 Asn Cys Ile Val Asn Val Cys Gln Cys Lys Pro Gly Phe Lys Arg Gly
     882          50                  55                  60
     883 Pro Lys Gly Cys Val Ala Pro Gly Pro Gly Cys Lys
     884 65                  70                  75
    1121 <210> SEQ ID NO: 36
    1122 <211> LENGTH: (686) 685 (p 8)
    1123 <212> TYPE: DNA
    1124 <213> ORGANISM: Ancyclostoma caninum
    1126 <220> FEATURE:
    1127 <221> NAME/KEY: CDS
    1128 <222> LOCATION: (14)..(556)
    1130 <220> FEATURE:
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Input Set : A:\PTO.VSK.txt
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```
       1131 <221> NAME/KEY: misc_feature
       1132 <223> OTHER INFORMATION:
       1134 <400> SEQUENCE: 36
E--> 1136 aattccgga aaa atg ctg atg ctc tac ctt gtt cct atc tgg ttg cta   48
     1137             Met Leu Met Leu Tyr Leu Val Pro Ile Trp Leu Leu
     1138              1               5                  10
E--> 1139 ctc att tcg caa tgc agt gga aaa tcc gcg aag aaa tgt ggt ctc aat   97
     1140 Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys Lys Cys Gly Leu Asn
     1141          15              20                  25
E--> 1142 gaa aaa ttg gac tgt ggc aat ctg aag gca tgc gag aaa aag tgc agc  145
     1143 Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser
     1144          30              35                  40
E--> 1145 gac ttg gac aat gag gag gat tat aag gag gaa gat gag tcg aaa tgc  193
     1146 Asp Leu Asp Asn Glu Glu Asp Tyr Lys Glu Glu Asp Glu Ser Lys Cys
     1147 45                  50                  55                  60
E--> 1148 cga tca cgt gaa tgt agt cgt cgt gtt tgt gta tgc gat gaa gga ttc  241
     1149 Arg Ser Arg Glu Cys Ser Arg Arg Val Cys Val Cys Asp Glu Gly Phe
W--> 1150              65                  70
E--> 1151 tac aga aac aag aag ggc caa tgt gtg aca aga gat gat tgc gag tat  289
     1152 Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp Asp Cys Glu Tyr
     1153              80                  85                  90
E--> 1154 gac aat atg gag att atc act ttt cca cca gaa gat aaa tgt ggt ccc  337
     1155 Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Lys Cys Gly Pro
W--> 1156              95                 100                 101
E--> 1157 gat gaa tgg ttc gac tgg tgt gga act tac aag cag tgt gag cgc aag  385
     1158 Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys Gln Cys Glu Arg Lys
     1159         110                 115                 120
E--> 1160 tgc aat aag gag cta agt gag aaa gat gaa gag gca tgc ctc tca cgt  433
     1161 Cys Asn Lys Glu Leu Ser Glu Lys Asp Glu Glu Ala Cys Leu Ser Arg
W--> 1162 125                 130                 135
E--> 1163 gct tgt act ggt cgt gct tgt gtt tgc aac gac gga ctg tac aga gac  481
     1164 Ala Cys Thr Gly Arg Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp
     1165             145                 150                 155
E--> 1166 gat ttt ggc aat tgt gtt gag aaa gac gaa tgt aac gat atg gag att  529
     1167 Asp Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile
     1168             160                 165                 170
E--> 1169 atc act ttt cca ccg gaa acc aaa cac tgaccaaagg ctctaactct cgctacat  584
     1170 Ile Thr Phe Pro Pro Glu Thr Lys His
     1171             175                 180
E--> 1173 aacgtcagtg cttgaattgc cccttacga gttagtaatt ttgaetaact ctgtgtaatt  644
E--> 1175 gagcattgtc tactgatggt gaaaatgaag tgttcaatgt ct  686
       1178 <210> SEQ ID NO: 37
       1179 <211> LENGTH: 707
       1180 <212> TYPE: DNA
       1181 <213> ORGANISM: Ancyclostoma caninum
       1183 <220> FEATURE:
       1184 <221> NAME/KEY: CDS
       1185 <222> LOCATION: (34)..(576)
       1187 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

[handwritten: use lower-case letters]

```
     1188 <221> NAME/KEY: misc_feature
     1189 <223> OTHER INFORMATION:
     1191 <400> SEQUENCE: 37
C--> 1193 gaattccgcg gaattccggt tggcggcaga aaa atg ctg atg ctc tac ctt gtt 54
     1194                                     Met Leu Met Leu Tyr Leu Val
     1195                                      1                   5
     1196 cct atc tgg ttc ctg ctc att tcg caa tgc agt gga aaa tcc gcg aag 102
     1197 Pro Ile Trp Phe Leu Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys
     1198          10                  15                  20
     1199 aaa tgt ggc ctc aat gaa aaa ttg gac tgt ggc aat ctg aag gca tgc 150
     1200 Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala Cys
     1201          25                  30                  35
     1202 gag aaa aag tgc agc gac ttg gac aat gag gag gat tat ggg gag gaa 198
     1203 Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp Tyr Gly Glu Glu
     1204 40                  45                  50                  55
     1205 gat gag tcg aaa tgc cga tca cgt gaa tgt att ggt cgt gtt tgc gta 246
     1206 Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ile Gly Arg Val Cys Val
     1207                  60                  65                  70
     1208 tgc gat gaa gga ttc tac aga aac aag aag ggc caa tgt gtg aca aga 294
     1209 Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg
     1210              75                  80                  85
     1211 gac gat tgc gag tat gac aat atg gag att atc act ttt cca cca gaa 342
     1212 Asp Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu
     1213              90                  95                  100
     1214 gat aaa tgt ggt ccc gat gaa tgg ttc gac tgg tgt gga act tac aag 390
     1215 Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys
     1216          105                 110                 115
E--> 1217 cag tgt gag cgc aag tgc agt gag gag cta aca gag aaa aat gag gag 438
     1218 Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser Glu Lys Asn Glu Glu
     1219 120                 125                 130                 135
     1220 gca tgc ctc tca cgt gct tgt act ggt cgt gct tgc gtt tgc aac gac 486
     1221 Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Asn Asp
     1222              140                 145                 150
     1223 gga ttg tat aga gac gat ttt ggc aat tgt gtt gag aaa gac gaa tgt 534
     1224 Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Glu Lys Asp Glu Cys
     1225              155                 160                 165
     1226 aac gat atg gag att atc act ttt cca ccg gaa agc aaa cac tgaccaaagg 586
W--> 1227 Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu (TSr) Lys His
     1228              170                 175                 180
     1230 ctctagctct cgctacataa cgtcagtgct tgaattgtcc ctttacgtgt tagtaatttt 646
     1232 gactaactct gtgtatttga gcattgtcta ctaatggtga aaatgaagct tttcaatgac 706
     1234 t 707
     1339 <210> SEQ ID NO: 41
     1340 <211> LENGTH: 75
     1341 <212> TYPE: PRT
     1342 <213> ORGANISM: Ancyclostoma caninum
     1345 <220> FEATURE:
     1346 <221> NAME/KEY: misc_feature
     1347 <223> OTHER INFORMATION:
```

[handwritten annotations: "invald" near line 1216; "invald" near line 1228; "p/o"]

RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
       1349 <400> SEQUENCE: 41
       1351 Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Val Cys Gly
E-->   1352  1  5 10 15          Misaligned nos.
       1353 Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu Glu Glu Glu Asp
E-->   1354  20 25 30
       1355 Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly Pro Ala Ala Cys Val Cys
E-->   1356  35 40 45
       1357 Glu Asp Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Lys Glu
E-->   1358  50 55 60
       1359 Glu Glu Cys Asp Gln His Glu Ile Ile His Val
E-->   1360  65 70 75
       1362 <210> SEQ ID NO: 42
       1363 <211> LENGTH: 74
       1364 <212> TYPE: PRT
       1365 <213> ORGANISM: Ancyclostoma caninum
       1368 <220> FEATURE:
       1369 <221> NAME/KEY: misc_feature
       1370 <223> OTHER INFORMATION:
       1372 <400> SEQUENCE: 42
       1374 Arg Thr Ala Arg Lys Pro Pro Thr Cys Gly Glu Asn Glu Arg Val Glu
E-->   1375  1  5 10 15          Misaligned
       1376 Trp Cys Gly Lys Glu Cys Glu Ile Thr Cys Asp Asp Pro Asp Lys Ile
E-->   1377  20 25 30
       1378 Cys Arg Ser Leu Ala Cys Pro Gly Pro Pro Ala Cys Val Cys Asp Asp
E-->   1379  35 40 45
       1380 Gly Tyr Tyr Arg Asp Thr Asn Val Gly Leu Cys Val Gln Tyr Asp Glu
E-->   1381  50 55 60
       1382 Cys Asn Asp Met Asp Ile Ile Met Val Ser
E-->   1383  65 70
       1385 <210> SEQ ID NO: 43
       1386 <211> LENGTH: 88
       1387 <212> TYPE: PRT
       1388 <213> ORGANISM: Ancyclostoma caninum
       1391 <220> FEATURE:
       1392 <221> NAME/KEY: misc_feature
       1393 <223> OTHER INFORMATION:
       1395 <400> SEQUENCE: 43
       1397 Lys Pro Ser Glu Lys Glu Cys Gly Pro His Glu Arg Leu Asp Cys Gly
E-->   1398  1  5 10 15          Misaligned
       1399 Asn Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu Glu
E-->   1400  20 25 30
       1401 Glu Asp Asp Tyr Glu Glu Gly Thr Glu Arg Phe Arg Cys Leu Leu Arg
E-->   1402  35 40 45
       1403 Val Cys Asp Glu Pro Tyr Glu Cys Ile Cys Asp Asp Gly Tyr Tyr Arg
E-->   1404  50 55 60
       1405 Asn Lys Lys Gly Glu Cys Val Thr Asp Asp Val Cys Glu Glu Asp Phe
E-->   1406  65 70 75 80
       1407 Met Glu Phe Ile Thr Phe Ala Pro
E-->   1408  85
```

RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
1409 <210> SEQ ID NO: 44
1410 <211> LENGTH: 87
1411 <212> TYPE: PRT
1412 <213> ORGANISM: Ancyclostoma caninum
1415 <220> FEATURE:
1416 <221> NAME/KEY: misc_feature
1417 <223> OTHER INFORMATION:
1419 <400> SEQUENCE: 44
1421 Arg Pro Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Ala Cys Gly Asn
E--> 1422   1  5 10 15
1423 Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu Glu Glu
E--> 1424   20 25 30
1425 Asp Asp Tyr Pro Glu Gly Thr Glu Arg Phe Arg Cys Leu Leu Arg Val
E--> 1426   35 40 45
1427 Cys Asp Gln Pro Tyr Glu Cys Ile Cys Asp Asp Gly Tyr Tyr Arg Asn
E--> 1428   50 55 60
1429 Lys Lys Gly Glu Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met
E--> 1430   65 70 75 80
1431 Glu Phe Ile Thr Phe Ala Pro
E--> 1432   85
1434 <210> SEQ ID NO: 45
1435 <211> LENGTH: 86
1436 <212> TYPE: PRT
1437 <213> ORGANISM: Ancyclostoma caninum
1440 <220> FEATURE:
1441 <221> NAME/KEY: misc_feature
1442 <223> OTHER INFORMATION:
1444 <400> SEQUENCE: 45
1446 Arg Pro Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn
E--> 1447   1  5 10 15
1448 Lys Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu Glu Glu
E--> 1449   20 25 30
1450 Asp Asp Asp Val Glu Asp Thr Asp Val Arg Cys Leu Val Arg Val Cys
E--> 1451   35 40 45
1452 Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp Gly Tyr Tyr Arg Asn Lys
E--> 1453   50 55 60
1454 Lys Gly Glu Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met Glu
E--> 1455   65 70 75 80
1456 Phe Ile Thr Phe Ala Pro
E--> 1457   85
1459 <210> SEQ ID NO: 46
1460 <211> LENGTH: 86
1461 <212> TYPE: PRT
1462 <213> ORGANISM: Ancyclostoma caninum
1464 <220> FEATURE:
1465 <221> NAME/KEY: misc_feature
1466 <223> OTHER INFORMATION:
1468 <400> SEQUENCE: 46
1470 Arg Pro Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn
```

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RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
E--> 1471  1  5 10 15        miselgrid nos.
     1472 Lys Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu Glu Glu
E--> 1473   20 25 30
     1474 Asp Asp Asp Val Glu Glu Thr Asp Val Arg Cys Leu Val Arg Val Cys
E--> 1475   35 40 45
     1476 Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp Gly Tyr Tyr Arg Asn Lys
E--> 1477   50 55 60
     1478 Lys Gly Glu Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met Glu
E--> 1479   65 70 75 80
     1480 Phe Ile Thr Phe Ala Pro
E--> 1481   85
     1483 <210> SEQ ID NO: 47
     1484 <211> LENGTH: 78
     1485 <212> TYPE: PRT
     1486 <213> ORGANISM: Ancyclostoma caninum
     1488 <220> FEATURE:
     1489 <221> NAME/KEY: misc_feature
     1490 <223> OTHER INFORMATION:
     1492 <400> SEQUENCE: 47
     1494 Lys Ser Leu Trp Asp Gln Lys Cys Gly Glu Asn Glu Arg Leu Asp Cys
E--> 1495  1  5 10 15      miselgred
     1496 Gly Asn Gln Lys Asp Cys Glu Arg Lys Cys Asp Asp Lys Arg Ser Glu
E--> 1497   20 25 30
     1498 Glu Glu Ile Met Gln Ala Cys Leu Thr Arg Gln Cys Leu Pro Pro Val
E--> 1499   35 40 45
     1500 Cys Val Cys Glu Asp Gly Phe Tyr Arg Asn Asp Asn Asp Gln Cys Val
E--> 1501   50 55 60
     1502 Asp Glu Glu Glu Cys Asn Met Glu Phe Ile Thr Phe Ala Pro
E--> 1503   65 70 75
     1506 <210> SEQ ID NO: 48
     1507 <211> LENGTH: 89
     1508 <212> TYPE: PRT
     1509 <213> ORGANISM: Ancyclostoma ceylanicum
     1511 <220> FEATURE:
     1512 <221> NAME/KEY: misc_feature
     1513 <223> OTHER INFORMATION:
     1515 <400> SEQUENCE: 48
     1517 Lys Pro Asn Asn Val Met Thr Asn Ala Cys Gly Leu Asn Glu Tyr Phe
E--> 1518  1  5 10 15      miselgred
     1519 Ala Glu Cys Gly Asn Met Lys Glu Cys Glu His Arg Cys Asn Glu Glu
E--> 1520   20 25 30
     1521 Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile Thr Ala Cys Leu Ile Arg
E--> 1522   35 40 45
     1523 Val Cys Phe Arg Pro Gly Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg
E--> 1524   50 55 60
     1525 Asn Arg Thr Gly Ser Cys Val Glu Glu Asp Asp Cys Glu Tyr Glu Asn
E--> 1526   65 70 75 80
     1527 Met Glu Phe Ile Thr Phe Ala Pro Glu
E--> 1528   85
```

RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
1530 <210> SEQ ID NO: 49
1531 <211> LENGTH: 82
1532 <212> TYPE: PRT
1533 <213> ORGANISM: Ancyclostoma ceylanicum
1535 <220> FEATURE:
1536 <221> NAME/KEY: misc_feature
1537 <223> OTHER INFORMATION:
1539 <400> SEQUENCE: 49
1541 Val Pro Ile Cys Gly Ser Asn Glu Arg Tyr Ser Asp Cys Gly Asn Asp
1542    1    5   10   15
1543 Lys Gln Cys Glu Arg Lys Cys Asn Glu Asp Asp Tyr Glu Lys Gly Asp
1544       20   25   30
1545 Glu Ala Cys Arg Ser His Val Cys Glu Arg Pro Gly Ala Cys Val Cys
1546       35   40   45
1547 Glu Asp Gly Phe Tyr Arg Asn Lys Lys Gly Ser Cys Val Glu Ser Asp
1548       50   55   60
1549 Asp Cys Glu Tyr Asp Asn Met Asp Phe Ile Thr Phe Ala Pro Glu Thr
1550   65   70   75   80
1551 Ser Arg
1553 <210> SEQ ID NO: 50
1554 <211> LENGTH: 84
1555 <212> TYPE: PRT
1556 <213> ORGANISM: Ancyclostoma caninum
1558 <220> FEATURE:
1559 <221> NAME/KEY: misc_feature
1560 <223> OTHER INFORMATION:
1562 <400> SEQUENCE: 50
1564 Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn
1565    1    5   10   15
1566 Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp
1567       20   25   30
1568 Tyr Lys Gln Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser Arg
1569       35   40   45
1570 Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Gln
1571       50   55   60
1572 Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr
1573   65   70   75   80
1574 Phe Pro Pro Glu
1576 <210> SEQ ID NO: 51
1577 <211> LENGTH: 84
1578 <212> TYPE: PRT
1579 <213> ORGANISM: Ancyclostoma caninum
1581 <220> FEATURE:
1582 <221> NAME/KEY: misc_feature
1583 <223> OTHER INFORMATION:
1585 <400> SEQUENCE: 51
1587 Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn
1588    1    5   10   15
1589 Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp
```

E--> 1542, E--> 1544, E--> 1546, E--> 1548, E--> 1550, E--> 1565, E--> 1567, E--> 1569, E--> 1571, E--> 1573, E--> 1588

RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
E-->  1590  20  25  30                  misaligned
      1591 Tyr Gly Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ile Gly
E-->  1592  35  40  45
      1593 Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Gln
E-->  1594  50  55  60
      1595 Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr
E-->  1596  65  70  75  80
      1597 Phe Pro Pro Glu
      1599 <210> SEQ ID NO: 52
      1600 <211> LENGTH: 83
      1601 <212> TYPE: PRT
      1602 <213> ORGANISM: Ancyclostoma duodenale
      1604 <220> FEATURE:
      1605 <221> NAME/KEY: misc_feature
      1606 <223> OTHER INFORMATION:
      1608 <400> SEQUENCE: 52
      1610 Lys Ala Ala Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys Gly Asn
E-->  1611  1   5  10  15              misaligned
      1612 Leu Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu Ser Glu Glu Tyr
E-->  1613  20  25  30
      1614 Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser Arg Arg
E-->  1615  35  40  45
      1616 Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Lys Cys
E-->  1617  50  55  60
      1618 Val Ala Lys Asp Val Cys Glu Asp Asp Asn Met Glu Ile Ile Thr Phe
E-->  1619  65  70  75  80
      1620 Pro Pro Glu
      1622 <210> SEQ ID NO: 53
      1623 <211> LENGTH: 78
      1624 <212> TYPE: PRT
      1625 <213> ORGANISM: Ancyclostoma caninum
      1627 <220> FEATURE:
      1628 <221> NAME/KEY: misc_feature
      1629 <223> OTHER INFORMATION:
      1631 <400> SEQUENCE: 53
      1633 Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys
E-->  1634  1   5  10  15              misaligned
      1635 Gln Cys Glu Arg Lys Cys Asn Lys Glu Leu Ser Glu Lys Asp Glu Glu
E-->  1636  20  25  30
      1637 Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Asn Asp
E-->  1638  35  40  45
      1639 Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Glu Lys Asp Glu Cys
E-->  1640  50  55  60
      1641 Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys His
E-->  1642  65  70  75
      1644 <210> SEQ ID NO: 54
      1645 <211> LENGTH: 78
      1646 <212> TYPE: PRT
      1647 <213> ORGANISM: Ancyclostoma caninum
```

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RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

        1649 <220> FEATURE:
        1650 <221> NAME/KEY: misc_feature
        1651 <223> OTHER INFORMATION:
        1653 <400> SEQUENCE: 54
        1655 Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys
E--> 1656   1 5 10 15   *misalpred*
        1657 Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser Glu Lys Asn Glu Glu
E--> 1658   20 25 30
        1659 Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Asn Asp
E--> 1660   35 40 45
        1661 Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Glu Lys Asp Glu Cys
E--> 1662   50 55 60
        1663 Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys His
E--> 1664   65 70 75
        1666 <210> SEQ ID NO: 55
        1667 <211> LENGTH: 77
        1668 <212> TYPE: PRT
        1669 <213> ORGANISM: Ancyclostoma duodenale
        1671 <220> FEATURE:
        1672 <221> NAME/KEY: misc_feature
        1673 <223> OTHER INFORMATION:
        1675 <400> SEQUENCE: 55
        1677 Lys Cys Pro Thr Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys His
E--> 1678   1 5 10 15   *misalpred nos.*
        1679 Cys Glu Leu Lys Cys Asp Arg Glu Leu Thr Glu Lys Glu Glu Gln Ala
E--> 1680   20 25 30
        1681 Cys Leu Ser Arg Val Cys Glu Lys Ser Ala Cys Val Cys Asn Asp Gly
E--> 1682   35 40 45
        1683 Leu Tyr Arg Asp Lys Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn
E--> 1684   50 55 60
        1685 Asp Met Glu Ile Ile Thr Phe Ala Pro Glu Glu Thr Lys
E--> 1686   65 70 75
        1688 <210> SEQ ID NO: 56
        1689 <211> LENGTH: 78
        1690 <212> TYPE: PRT
        1691 <213> ORGANISM: Ancyclostoma duodenale
        1694 <220> FEATURE:
        1695 <221> NAME/KEY: misc_feature
        1696 <223> OTHER INFORMATION:
        1698 <400> SEQUENCE: 56
        1700 Asp Glu Cys Gly Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr Lys
E--> 1701   1 5 10 15   *misalpred nos.*
        1702 Lys Cys Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys Asn Glu Glu
E--> 1703   20 25 30
        1704 Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Lys Asp
E--> 1705   35 40 45
        1706 Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Pro His Asp Glu Cys
E--> 1707   50 55 60
        1708 Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys His

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PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

```
E--> 1709  65 70 75
     1711 <210> SEQ ID NO: 57
     1712 <211> LENGTH: 75
     1713 <212> TYPE: PRT
     1714 <213> ORGANISM: Ancyclostoma ceylanicum
     1717 <220> FEATURE:
     1718 <221> NAME/KEY: misc_feature
     1719 <223> OTHER INFORMATION:
     1721 <400> SEQUENCE: 57
     1723 Lys Ala Phe Pro Lys Cys Asp Val Asn Glu Arg Phe Glu Val Cys Gly
E--> 1724  1 5 10 15
     1725 Asn Leu Lys Glu Cys Glu Leu Lys Cys Asp Glu Asp Pro Lys Ile Cys
E--> 1726  20 25 30
     1727 Ser Arg Ala Cys Ile Arg Pro Pro Ala Cys Val Cys Asp Asp Gly Phe
E--> 1728  35 40 45
     1729 Tyr Arg Asp Lys Tyr Gly Phe Cys Val Glu Glu Asp Glu Cys Asn Asp
E--> 1730  50 55 60
     1731 Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys
E--> 1732  65 70 75
     1734 <210> SEQ ID NO: 58
     1735 <211> LENGTH: 77
     1736 <212> TYPE: PRT
     1737 <213> ORGANISM: Ancyclostoma ceylanicum
     1740 <220> FEATURE:
     1741 <221> NAME/KEY: misc_feature
     1742 <223> OTHER INFORMATION:
     1744 <400> SEQUENCE: 58
     1746 Arg Thr Val Lys Lys Cys Gly Lys Asn Glu Arg Tyr Asp Asp Cys Gly
E--> 1747  1 5 10 15
     1748 Asn Ala Lys Asp Cys Glu Thr Lys Cys Gly Glu Glu Glu Lys Val Cys
E--> 1749  20 25 30
     1750 Arg Ser Arg Glu Cys Thr Ser Pro Gly Ala Cys Val Cys Glu Gln Gly
E--> 1751  35 40 45
     1752 Phe Tyr Arg Asp Pro Ala Gly Asp Cys Val Thr Asp Glu Glu Cys Asp
E--> 1753  50 55 60
     1754 Glu Trp Asn Asn Met Glu Ile Ile Thr Met Pro Lys Gln
E--> 1755  65 70 75
     1757 <210> SEQ ID NO: 59
     1758 <211> LENGTH: 84
     1759 <212> TYPE: PRT
     1760 <213> ORGANISM: Ancyclostoma caninum
     1763 <220> FEATURE:
     1764 <221> NAME/KEY: misc_feature
     1765 <223> OTHER INFORMATION:
     1767 <400> SEQUENCE: 59
     1769 Lys Ala Thr Met Gln Cys Gly Glu Asn Glu Lys Tyr Asp Ser Cys Gly
E--> 1770  1 5 10 15
     1771 Ser Lys Glu Cys Asp Lys Lys Cys Lys Tyr Asp Gly Val Glu Glu Glu
E--> 1772  20 25 30
```

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PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
      1773 Asp Asp Glu Glu Pro Asn Val Pro Cys Leu Val Arg Val Cys His Glu
E--> 1774 (35 40 45)
      1775 Asp Cys Val Cys Glu Glu Gly Phe Tyr Arg Asn Lys Asp Asp Lys Cys
E--> 1776 (50 55 60)
      1777 Val Ser Ala Glu Asp Cys Glu Leu Asp Asn Met Asp Phe Ile Tyr Pro
E--> 1778 (65 70 75 80)
      1779 Gly Thr Arg Asn
      2064 <210> SEQ ID NO: 72
      2065 <211> LENGTH: 5
      2066 <212> TYPE: PRT
W--> 2067 <213> ORGANISM:                  <- mandatory response
      2070 <220> FEATURE:
      2071 <221> NAME/KEY: misc_feature
      2072 <223> OTHER INFORMATION:
      2074 <400> SEQUENCE: 72              -> invalid
E--> 2076 Gly Tyr Tyr Arg Asn
E--> 2077 1 5    mistyped number
      2154 <210> SEQ ID NO: 78
      2155 <211> LENGTH: 5  7 <-
      2156 <212> TYPE: PRT        response needed
W--> 2157 <213> ORGANISM:
      2160 <220> FEATURE:
W--> 2161 <221> NAME/KEY: "Xaa" in locations 1 and 2 is an amino acid, provided that at
W--> 2162       least one Xaa is Glu or Asp
      2163 <223> OTHER INFORMATION: <-
      2165 <400> SEQUENCE: 78
W--> 2167 Xaa Xaa Gly Phe Tyr Arg Asp
E--> 2168 1 5   mistyped
      2319 <210> SEQ ID NO: 89
      2320 <211> LENGTH: 25  22
      2321 <212> TYPE: DNA          -> response needed
W--> 2322 <213> ORGANISM:
      2324 <400> SEQUENCE: 89      -> invalid
E--> 2326 aacccatacc cccactct cc tc 22
      2327 <210> SEQ ID NO: 90
      2328 <211> LENGTH: 21
      2329 <213> TYPE: PRT          -> response needed
W--> 2330 <213> ORGANISM:
      2333 <220> FEATURE:
W--> 2334 <221> NAME/KEY: "Xaa" in locations 1 to 2 is an amino acid
      2335 <223> OTHER INFORMATION:
      2337 <400> SEQUENCE: 90
E--> 2339 AARCCNTGYG ARMGGAARTG Y 21
      2341 <210> SEQ ID NO: 91
      2342 <211> LENGTH: 23 <-
      2343 <212> TYPE: PRT <-
      2344 <213> ORGANISM: Ancyclostoma caninum
      2346 <220> FEATURE:
W--> 2347 <221> NAME/KEY: "W" stands for A or T; "R" stands for A of G; "N" stands for any
```

Handwritten annotations:

It is already understood that Xaa is an amino acid.

any amino acid? (Explain further)

Xaa can only represent an amino acid

move to <223> line

These are bases, with cumulative base total. (Per <212>) This is a peptide sequence

This is a peptide sequence!

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PATENT APPLICATION: US/09/498,556A   TIME: 11:49:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

W--> 2348   base; and "Y" stands for C or T.   ?
     2349 <223> OTHER INFORMATION:
     2351 <400> SEQUENCE: 91
E--> 2353 TWRWANCCNT CYTTRCANAC RCA 23   ?
     2354 <210> SEQ ID NO: 92
     2355 <211> LENGTH: 13
     2356 <212> TYPE: PRT
     2357 <213> ORGANISM: Ancyclostoma caninum
     2359 <220> FEATURE:
     2360 <221> NAME/KEY: misc_feature
     2361 <223> OTHER INFORMATION:
     2363 <400> SEQUENCE: 92
E--> 2365 Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu (Aop) invalid
     2366   1 .   5   .   10
     2380 <210> SEQ ID NO: 94
     2381 <211> LENGTH: (28) 33
     2382 <212> TYPE: DNA
     2383 <213> ORGANISM: Ancyclostoma caninum
     2385 <220> FEATURE:
W--> 2386 <221> NAME/KEY: "R" stands for A or G; "N" stands for inosine; "Y" stands for C
W--> 2387   or T
     2388 <223> OTHER INFORMATION: goes on <223> line
     2390 <400> SEQUENCE: 94
E--> 2392 aargcntayc cngartgygg ngaraaygar tgg 33
     2417 <210> SEQ ID NO: 97
     2418 <211> LENGTH: 20
     2419 <212> TYPE: PRT
     2420 <213> ORGANISM: Ancyclostoma caninum
     2422 <220> FEATURE:
     2423 <221> NAME/KEY: misc_feature
     2424 <223> OTHER INFORMATION: N-terminal caninum
     2426 <400> SEQUENCE: 97
E--> 2428 Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu (Tip) Leu Asp Asp Cys Gly Thr   invalid
     2429   1 invalid   5   10   15
E--> 2430 (Gb) Lys Pro
     2431   20
     2529 <210> SEQ ID NO: 106
     2530 <211> LENGTH: (36) 5 shown below
     2531 <212> TYPE: PRT
     2532 <213> ORGANISM: Ancyclostoma caninum
     2534 <220> FEATURE:
     2535 <221> NAME/KEY: misc_feature
     2536 <223> OTHER INFORMATION: N-terminal fragment
     2538 <400> SEQUENCE: 106
     2540 Lys Ala Tyr Pro Glu
E--> 2541   1   5
     2799 <210> SEQ ID NO: 128
     2800 <211> LENGTH: 91   p19
     2801 <212> TYPE: PRT

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Input Set : A:\PTO.VSK.txt
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```
        2802 <213> ORGANISM: Ancyclostoma caninum
        2804 <220> FEATURE:
        2805 <221> NAME/KEY: misc_feature
        2806 <223> OTHER INFORMATION:
        2808 <400> SEQUENCE: 128
E-->    2810 Leu Val Ear Tyr Cys Ser Gly Lys Ala Thr Met Gln Cys Gly Glu Asn
        2811  1           5               10              15
        2812 Glu Lys Tyr Asp Ser Cys Gly Ser Lys Glu Cys Asp Lys Lys Cys Lys
        2813          20              25              30
        2814 Tyr Asp Gly Val Glu Glu Glu Asp Asp Glu Glu Pro Asn Val Pro Cys
        2815          35              40              45
        2816 Leu Val Arg Val Cys His Gln Asn Cys Val Cys Glu Glu Gly Phe Tyr
        2817      50              55              60
        2818 Arg Asn Lys Asp Asp Lys Cys Val Ser Ala Glu Asp Cys Glu Leu Asp
        2819 65              70              75              80
        2820 Asn Met Asp Phe Ile Tyr Pro Gly Thr Arg Asn
        2821              85              90
        2848 <210> SEQ ID NO: 131
        2849 <211> LENGTH: 6
        2850 <212> TYPE: DNA
W-->    2851 <213> ORGANISM:
        2853 <220> FEATURE:
W-->    2854 <221> NAME/KEY: Xaa in location 2 to 5 is an amino acid
        2855 <223> OTHER INFORMATION: Internal fragment
        2857 <400> SEQUENCE: 131
W-->    2859 Cys Xaa Xaa Xaa Xaa Cys
E-->    2860  1           5
        3425 <210> SEQ ID NO: 174
        3426 <211> LENGTH: 20
        3427 <212> TYPE: PRT
W-->    3428 <213> ORGANISM:
        3430 <220> FEATURE:
W-->    3431 <221> NAME/KEY: Xaa in locations 2 to 5 is an amino acid
        3432 <223> OTHER INFORMATION: Internal fragment
        3434 <400> SEQUENCE: 174
W-->    3436 Cys Xaa Xaa Xaa Xaa
E-->    3437  1           5
        3438 <210> SEQ ID NO: 175
        3439 <211> LENGTH: 20
        3440 <212> TYPE: PRT
W-->    3441 <213> ORGANISM:
        3443 <220> FEATURE:
W-->    3444 <221> NAME/KEY: Xaa in locations 2 to 4 is an amino acid
        3445 <223> OTHER INFORMATION: Internal fragment
        3447 <400> SEQUENCE: 175
W-->    3449 Cys Xaa Xaa Xaa
E-->    3450  1
E-->    3490 <210> SEQ ID NO: 180
        3491 <211> LENGTH: 14
```

[Handwritten annotations:]
invalid (Please ensure all amino acids are properly listed)

<212> response is DNA.

? Why are amino acids shown below?

mandatory response

explain in another <223> line

? 5 shown below

mandatory response

Explain further; Xaa can only be an amino acid, anyway.

Explain further. Show explanation on <223>

Explain further. Show explanation on <223> line, not on <221> line.

same err

15 (p. 20)

Sequence 179 Missing

same err

response needed ← shown

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Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

```
        3492 <212> TYPE: PRT                                    → response needed        → what about 15?
W-->    3493 <213> ORGANISM:
        3495 <220> FEATURE:
W-->    3496 <221> NAME/KEY: Xaa in locations 2 and locations 4 to 14 is an amino acid
        3497 <223> OTHER INFORMATION: Internal fragment
        3499 <400> SEQUENCE: 180
W-->    3501 Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E-->    3502 1               5                   10              15
        3503 <210> SEQ ID NO: 181                                           see previous
        3504 <211> LENGTH: 8  14                                            page on
        3505 <212> TYPE: PRT                                                how to
W-->    3506 <213> ORGANISM:                                                edit this
        3508 <220> FEATURE:
W-->    3509 <221> NAME/KEY: Xaa in locations 2 to 8 is an amino acid      edit
        3510 <223> OTHER INFORMATION: Internal fragment
        3512 <400> SEQUENCE: 181
W-->    3514 Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa      → Xaa's are at
E-->    3515 1               5                   10                          location 9-14
        3516 <210> SEQ ID NO: 182
        3517 <211> LENGTH: 7  8
        3518 <213> TYPE: PRT
W-->    3519 <213> ORGANISM:
        3521 <220> FEATURE:
W-->    3522 <221> NAME/KEY: Xaa in locations 2 to 7 is an amino acid       edit per
        3523 <223> OTHER INFORMATION: Internal fragment                     above
        3525 <400> SEQUENCE: 182
W-->    3527 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E-->    3528 1               5
        3529 <210> SEQ ID NO: 183
        3530 <211> LENGTH: 6  7
        3531 <212> TYPE: PRT
W-->    3532 <213> ORGANISM:
        3534 <220> FEATURE:
W-->    3535 <221> NAME/KEY: Xaa in locations 2 to 6 is an amino acid       edit
        3536 <223> OTHER INFORMATION: Internal fragment
        3538 <400> SEQUENCE: 183
W-->    3540 Cys Xaa Xaa Xaa Xaa Xaa Xaa
E-->    3541 1               5                                          ?
        3542 <210> SEQ ID NO: 184
        3543 <211> LENGTH: 26  6
        3544 <212> TYPE: PRT
W-->    3545 <213> ORGANISM:                                             same
        3547 <220> FEATURE:                                              typed
W-->    3548 <221> NAME/KEY: Xaa in locations 2 to 26 is an amino acid   error
        3549 <223> OTHER INFORMATION: Internal fragment                 in Seq. 185-204
        3551 <400> SEQUENCE: 184                                        and in Seq. 248-257
W-->    3553 Cys Xaa Xaa Xaa Xaa Xaa
E-->    3554 1               5
E-->    3832 <210> SEQ ID NO: 204
```

↓ Seq. 204 is shown twice which one is correct?

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Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04262002\I498556A.raw

```
E--> 3884 <210> SEQ ID NO: 207   ← shown twice
E--> 3897 <210> SEQ ID NO: 209   ← seq. 208 missing
     4220 <210> SEQ ID NO: 233
     4221 <211> LENGTH: 26
     4222 <212> TYPE: PRT
W--> 4223 <213> ORGANISM:
     4225 <220> FEATURE:
W--> 4226 <221> NAME/KEY: Xaa in location 2 to 26 is an amino acid      put in <223>
     4227 <223> OTHER INFORMATION: Internal fragment
     4229 <400> SEQUENCE: 233
W--> 4231 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     4232   1               5                   10                  15
E--> 4233 Xaa Xaa Xaa Xaa Xaa Xee Xaa Xaa Xaa Xaa         invalid
     4234               20              25
     4235 <210> SEQ ID NO: 234
     4236 <211> LENGTH: 25
     4237 <212> TYPE: PRT
W--> 4238 <213> ORGANISM:
     4240 <220> FEATURE:
W--> 4241 <221> NAME/KEY: Xaa in location 2 to 25 is an amino acid      put in <223>
     4242 <223> OTHER INFORMATION: Internal fragment
     4244 <400> SEQUENCE: 234
W--> 4246 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     4247                 5                   10                  15
E--> 4248 Xee Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa    invalid
     4249                20              25
E--> 4454 <210> SEQ ID NO: 248   → shown twice
E--> 4561 <210> SEQ ID NO: 257   → seq 256 missing
E--> 4717 <210> SEQ ID NO: 269   → seq. 268 missing
     4821 <210> SEQ ID NO: 277
     4822 <211> LENGTH: 15
     4823 <212> TYPE: PRT
W--> 4824 <213> ORGANISM:                                         edit
     4826 <220> FEATURE:
W--> 4827 <221> NAME/KEY: Xaa in location 2 and locations 4 to 15 is an amino acid
     4828 <223> OTHER INFORMATION: Internal fragment
     4830 <400> SEQUENCE: 277                invalid        delete
E--> 4832 Cys Xaa Cys Xaa Xaa Xaa Xaa Esa Xaa Xaa Xaa Xaas Xaa Xaa Xaa
E--> 4833   1  5  10 15    misaligned
     5349 <210> SEQ ID NO: 315
     5350 <211> LENGTH: 20
     5351 <212> TYPE: PRT                                         edit
W--> 5352 <213> ORGANISM:
     5354 <220> FEATURE:
W--> 5355 <221> NAME/KEY: Xaa in locations 1 to 3 and locations 5 to 20 is an amino acid
     5356 <223> OTHER INFORMATION: Internal fragment
     5358 <400> SEQUENCE: 315                          invalid
E--> 5360 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Eas Xaa Xaa Xaa Xaa
E--> 5361  .1  5  10 15        misaligned nos.
```

```
        RAW SEQUENCE LISTING              DATE: 04/26/2002
        PATENT APPLICATION:  US/09/498,556A    TIME: 11:49:43

           Input Set : A:\PTO.VSK.txt
           Output Set: N:\CRF3\04262002\I498556A.raw

W--> 5362 Xaa Xaa Xaa Xaa
E--> 5363 20  misaligned
     5904 <210> SEQ ID NO: 356
     5905 <211> LENGTH: 6
     5906 <212> TYPE: PRT
W--> 5907 <213> ORGANISM:                                    edit
     5909 <220> FEATURE:
W--> 5910 <221> NAME/KEY: Xaa in location 2 to 6 is an amino acid
     5911 <223> OTHER INFORMATION: Internal fragment
     5913 <400> SEQUENCE: 356
W--> 5915 Cys Xaa Xaa Xaa Xaa Xaa
E--> 5916 1 5  misaligned
E--> 5920 (. continued)
E--> 5921 (. continued)
E--> 5922 C:\WINNT\Profiles\chipman_1\Desktop\70016337_1.DOC
```

delete

see next page for more error

```
<210>  255      6 shown
<211>  (7)
<212>   PRT
<213>

<220>
<221>  Xaa in location 2 to 6 is an amino acid
<223>   Internal fragment

<400>   255

Cys Xaa Xaa Xaa Xaa Cys
 1                    5

Cys Xaa Xaa Xaa Cys
 1
```

Explain further and move to <223>, line

what is this?

FYI

5

24

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

Skipped Sequences(NEW_RULES):
Sequence(s)__missing. If intentional, please use the following format for
each skipped sequence.
<210> sequence id number
<400> sequence id number
000

Seq#:179,208,256,268

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/498,556A**

DATE: 04/26/2002
TIME: 11:49:44

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

```
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:49 M:201 W: Mandatory field data missing, <213> ORGANISM
L:53 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:64 M:201 W: Mandatory field data missing, <213> ORGANISM
L:68 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:72 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:91 M:112 C: (48) String data converted to lower case,
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:94 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:112 Repeated in SeqNo=3
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:98 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:100 M:254 E: No. of Bases conflict, LENGTH:Input:195 Counted:194 SEQ:3
L:100 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
M:254 Repeated in SeqNo=3
L:103 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:106 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:109 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:112 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:114 M:252 E: No. of Seq. differs, <211> LENGTH:Input:461 Found:460 SEQ:3
L:124 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:151 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=5
L:170 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:229 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:247 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=9
L:260 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:306 M:112 C: (48) String data converted to lower case,
L:307 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 10, CDS LOCATION:1..291
```

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

M:112 Repeated in SeqNo=10
L:312 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:317 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:347 M:112 C: (48) String data converted to lower case,
L:348 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:349 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
M:112 Repeated in SeqNo=11
L:352 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:361 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:390 M:112 C: (48) String data converted to lower case,
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
M:112 Repeated in SeqNo=12
L:396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:429 M:112 C: (48) String data converted to lower case,
L:431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
M:112 Repeated in SeqNo=13
L:434 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:437 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:442 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:446 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:459 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:530 SEQ:13
L:461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:484 M:112 C: (48) String data converted to lower case,
L:487 M:254 E: No. of Bases conflict, LENGTH:Input:105 Counted:102 SEQ:14
M:112 Repeated in SeqNo=14
L:489 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
M:254 Repeated in SeqNo=14
L:492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:495 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:501 M:252 E: No. of Seq. differs, <211> LENGTH:Input:349 Found:301 SEQ:14
L:519 M:112 C: (48) String data converted to lower case,

```
L:520 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
M:112 Repeated in SeqNo=15
L:561 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=16
L:603 M:112 C: (48) String data converted to lower case,
L:604 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 17, CDS LOCATION:1..291
M:112 Repeated in SeqNo=17
L:610 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:628 M:252 E: No. of Seq. differs, <211> LENGTH:Input:425 Found:434 SEQ:17
L:633 M:201 W: Mandatory field data missing, <213> ORGANISM
L:650 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:655 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=19
L:677 M:252 E: No. of Seq. differs, <211> LENGTH:Input:425 Found:430 SEQ:19
L:684 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:18
L:762 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:23
L:767 M:252 E: No. of Seq. differs, <211> LENGTH:Input:96 Found:0 SEQ:23
L:879 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:889 M:201 W: Mandatory field data missing, <213> ORGANISM
L:893 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=30
L:917 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=31
L:961 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=32
L:1005 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=33
L:1048 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=34
L:1092 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=35
L:1136 M:254 E: No. of Bases conflict, LENGTH:Input:49 Counted:48 SEQ:36
M:112 Repeated in SeqNo=36
M:254 Repeated in SeqNo=36
L:1150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:36
L:1156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:36
L:1162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:36
L:1175 M:252 E: No. of Seq. differs, <211> LENGTH:Input:686 Found:685 SEQ:36
L:1193 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=37
L:1217 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1227 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1251 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=38
L:1295 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=39
L:1352 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
M:332 Repeated in SeqNo=41
L:1375 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
```

```
M:332 Repeated in SeqNo=42
L:1398 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
M:332 Repeated in SeqNo=43
L:1422 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
M:332 Repeated in SeqNo=44
L:1447 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
M:332 Repeated in SeqNo=45
L:1471 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:1495 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
M:332 Repeated in SeqNo=47
L:1518 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:48
M:332 Repeated in SeqNo=48
L:1542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:49
M:332 Repeated in SeqNo=49
L:1565 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:50
M:332 Repeated in SeqNo=50
L:1588 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:51
M:332 Repeated in SeqNo=51
L:1611 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:52
M:332 Repeated in SeqNo=52
L:1634 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:53
M:332 Repeated in SeqNo=53
L:1656 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54
M:332 Repeated in SeqNo=54
L:1678 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:55
M:332 Repeated in SeqNo=55
L:1701 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:56
M:332 Repeated in SeqNo=56
L:1724 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:57
M:332 Repeated in SeqNo=57
L:1747 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:58
M:332 Repeated in SeqNo=58
L:1770 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:59
M:332 Repeated in SeqNo=59
L:1793 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:60
M:332 Repeated in SeqNo=60
L:1814 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61
M:332 Repeated in SeqNo=61
L:1835 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:62
M:332 Repeated in SeqNo=62
L:1870 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:63
M:332 Repeated in SeqNo=63
L:1904 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:64
M:332 Repeated in SeqNo=64
L:1962 M:201 W: Mandatory field data missing, <213> ORGANISM
L:1969 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:66
L:1975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0
L:1982 M:201 W: Mandatory field data missing, <213> ORGANISM
```

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

```
L:1989 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:67
L:1994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0
L:2000 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2007 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:68
L:2008 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:68
L:2009 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:68
L:2014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
L:2020 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2035 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2050 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2067 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2076 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:2082 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2098 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2113 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2127 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2142 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2157 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2161 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:78
L:2162 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:78
L:2167 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:78
L:2167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:0
L:2168 M:252 E: No. of Seq. differs, <211> LENGTH:Input:5 Found:7 SEQ:78
L:2173 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2177 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:79
L:2178 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:79
L:2183 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:79
L:2183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:2189 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2193 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:80
L:2194 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:80
L:2199 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:80
L:2199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:0
L:2205 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2209 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:81
L:2210 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:81
L:2215 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:81
L:2215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
L:2221 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2225 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:82
L:2226 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:82
L:2231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:82
L:2231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
L:2237 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2241 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:83
L:2246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:83
L:2246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
L:2252 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2256 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:84
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L:2257 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:84
L:2258 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:84
L:2263 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:84
L:2263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
L:2269 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2273 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:85
L:2278 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:85
L:2278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0
L:2284 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2288 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:86
L:2293 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:86
L:2293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:2299 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2303 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:87
L:2308 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:87
L:2308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
L:2314 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2318 M:112 C: (48) String data converted to lower case,
L:2322 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2326 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:2326 M:112 C: (48) String data converted to lower case,
L:2326 M:252 E: No. of Seq. differs, <211> LENGTH:Input:25 Found:22 SEQ:89
L:2330 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2334 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:90
L:2339 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:0 SEQ:90
L:2347 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:91
L:2348 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:91
L:2353 M:252 E: No. of Seq. differs, <211> LENGTH:Input:23 Found:0 SEQ:91
L:2365 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:2386 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:94
L:2387 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:94
L:2392 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:94
L:2392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:94 after pos.:0
L:2392 M:112 C: (48) String data converted to lower case,
L:2392 M:252 E: No. of Seq. differs, <211> LENGTH:Input:28 Found:33 SEQ:94
L:2408 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2428 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:2430 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2430 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:2541 M:252 E: No. of Seq. differs, <211> LENGTH:Input:36 Found:5 SEQ:106
L:2607 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2618 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2630 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2642 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2654 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2666 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2678 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2681 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:118
L:2686 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:118
```

VERIFICATION SUMMARY

PATENT APPLICATION: **US/09/498,556A**

DATE: 04/26/2002
TIME: 11:49:44

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

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L:2686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118 after pos.:0
L:2691 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2694 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:119
L:2695 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ
ID#:119
L:2696 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ
ID#:119
L:2701 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:119
L:2701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119 after pos.:0
L:2706 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2718 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2730 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2742 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2754 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2766 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2774 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:2778 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2790 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2798 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:2810 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:2825 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2828 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:129
L:2833 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:129
L:2833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129 after pos.:0
L:2838 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2846 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:130
L:2846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130 after pos.:0
L:2851 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2854 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:131
L:2859 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:131
L:2859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:0
L:2860 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:0 SEQ:131
L:2864 M:201 W: Mandatory field data missing, <213> ORGANISM
L:2867 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:132
L:2872 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:132
L:2872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:0
L:2880 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:133
L:2885 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:133
L:2885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:0
L:2893 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:134
L:2898 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:134
L:2898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134 after pos.:0
L:2900 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:134
L:2900 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134 after pos.:16
L:2908 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:135
L:2913 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:135
L:2913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:0
L:2915 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:135
L:2915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:16
L:2923 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:136
L:2928 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:136
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L:2928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136 after pos.:0
L:2930 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:136
L:2930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136 after pos.:16
L:2937 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:137
L:2942 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:137
L:2942 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:0
L:2944 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:137
L:2944 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:16
L:2951 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:138
L:2956 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:138
L:2956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0
L:2958 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:138
L:2958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:16
L:2965 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:139
L:2970 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:139
L:2970 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:2978 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:140
L:2983 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:140
L:2983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:2991 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:141
L:2996 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:141
L:2996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:3004 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:142
L:3009 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:142
L:3009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:3017 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:143
L:3022 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:143
L:3022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:0
L:3030 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:144
L:3035 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:144
L:3035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:0
L:3043 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:145
L:3048 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:145
L:3048 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145 after pos.:0
L:3056 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:146
L:3061 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:146
L:3061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:0
L:3069 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:147
L:3074 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:147
L:3074 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147 after pos.:0
L:3087 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:148
L:3087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:148 after pos.:0
L:3100 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:149
L:3100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:149 after pos.:0
L:3113 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:150
L:3113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:150 after pos.:0
L:3126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:151
L:3126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:151 after pos.:0
L:3139 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:152
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/498,556A

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TECH CENTER 1600 2900

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

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L:3139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152 after pos.:0
L:3152 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:153
L:3152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:153 after pos.:0
L:3165 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:154
L:3165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154 after pos.:0
L:3178 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:155
L:3178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:155 after pos.:0
L:3191 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:156
L:3191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:156 after pos.:0
L:3204 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:157
L:3204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:157 after pos.:0
L:3217 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:158
L:3230 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:159
L:3243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:160
L:3437 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:5 SEQ:174
L:3450 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:4 SEQ:175
L:3490 M:214 E: (33) Seq.# missing, SEQ ID NO:179
L:3502 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:15 SEQ:180
L:3515 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:14 SEQ:181
L:3528 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:8 SEQ:182
L:3541 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:7 SEQ:183
L:3554 M:252 E: No. of Seq. differs, <211> LENGTH:Input:26 Found:6 SEQ:184
L:3569 M:252 E: No. of Seq. differs, <211> LENGTH:Input:25 Found:26 SEQ:185
L:3584 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:25 SEQ:186
L:3599 M:252 E: No. of Seq. differs, <211> LENGTH:Input:23 Found:24 SEQ:187
L:3614 M:252 E: No. of Seq. differs, <211> LENGTH:Input:22 Found:23 SEQ:188
L:3629 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:22 SEQ:189
L:3644 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:21 SEQ:190
L:3659 M:252 E: No. of Seq. differs, <211> LENGTH:Input:19 Found:20 SEQ:191
L:3673 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:19 SEQ:192
L:3687 M:252 E: No. of Seq. differs, <211> LENGTH:Input:17 Found:18 SEQ:193
L:3701 M:252 E: No. of Seq. differs, <211> LENGTH:Input:16 Found:17 SEQ:194
L:3714 M:252 E: No. of Seq. differs, <211> LENGTH:Input:15 Found:16 SEQ:195
L:3727 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:15 SEQ:196
L:3740 M:252 E: No. of Seq. differs, <211> LENGTH:Input:13 Found:14 SEQ:197
L:3753 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:13 SEQ:198
L:3766 M:252 E: No. of Seq. differs, <211> LENGTH:Input:11 Found:12 SEQ:199
L:3779 M:252 E: No. of Seq. differs, <211> LENGTH:Input:10 Found:11 SEQ:200
L:3792 M:252 E: No. of Seq. differs, <211> LENGTH:Input:9 Found:10 SEQ:201
L:3805 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:202
L:3818 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:8 SEQ:203
L:3831 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:7 SEQ:204
L:3832 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:204
L:3884 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:207
L:3896 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:5 SEQ:207
L:3897 M:214 E: (33) Seq.# missing, SEQ ID NO:208
L:4233 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:4248 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:4454 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:248
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Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\04262002\I498556A.raw**

```
L:4466 M:252 E: No. of Seq. differs, <211> LENGTH:Input:11 Found:10 SEQ:248
L:4479 M:252 E: No. of Seq. differs, <211> LENGTH:Input:10 Found:9 SEQ:249
L:4492 M:252 E: No. of Seq. differs, <211> LENGTH:Input:9 Found:8 SEQ:250
L:4505 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:7 SEQ:251
L:4518 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:6 SEQ:252
L:4531 M:252 E: No. of Seq. differs, <211> LENGTH:Input:16 Found:8 SEQ:253
L:4544 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:7 SEQ:254
L:4560 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:11 SEQ:255
L:4561 M:214 E: (33) Seq.# missing, SEQ ID NO:256
L:4575 M:252 E: No. of Seq. differs, <211> LENGTH:Input:5 Found:23 SEQ:257
L:4717 M:214 E: (33) Seq.# missing, SEQ ID NO:268
L:4832 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:4832 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:5360 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:5920 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:5920 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2
L:5921 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:5921 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2
L:5922 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:5922 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
```
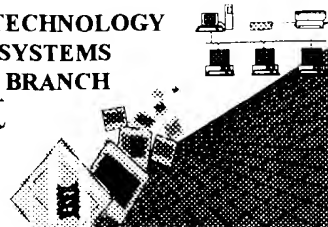
BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/498,556A_

Source: _OIPE_

Date Processed by STIC: _4/26/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
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TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
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   　　　Or
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Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	**SUGGESTED CORRECTION**	**SERIAL NUMBER:** C 9/498,556A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _/_ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _/_ ~~Invalid~~ *No* <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.